

Table 10 shows sequence alignment between a NOV3 polypeptide with various fibromodulins: ACC NO: O43408 (SEQ ID NO:61), ACC NO: AP000597 (SEQ ID NO:7), ACC NO: O43155 (SEQ ID NO:62), ACC NO: O42235 (SEQ ID NO:63) and FMOD Bovin FM (SEQ ID NO:64). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

Insert the sequence listing pages 1 - 42 at the end of the specification.

REMARKS

The specification has been amended throughout to insert SEQ ID NO:34 – SEQ ID NO:64 which were omitted by typographical error and to insert the sequence listing. Applicants submit that the above amendments add no new matter.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned “**Version with markings to show changes made.**”

Applicants believe that no fee is due with the submission of this Preliminary Amendment. However, the Commissioner is hereby authorized to charge any additional fees that may be due, or credit any overpayment of same, to Deposit Account No. 50-0311, Attorney Reference No. 15966-585A (Cura-85A).

CONCLUSION


On the basis of the foregoing amendment and remark, Applicants respectfully submit that the pending claims are in condition for allowance. Should any questions or issues arise

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concerning this application, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Respectfully submitted,

 42,867

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Version with markings to show changes made

In the Specification:

Table 2 on page 9 has been amended as follows:

Table 2.

Comparison between a NOV1 polypeptide and thymosin beta-10 from human

```
>gb|AAA36746.1| (M92383) thymosin beta-10 [Homo sapiens]
      Length = 49

Score = 84.5 bits (192), Expect = 3e-16
Identities = 34/40 (85%), Positives = 36/40 (90%), Gaps = 1/40 (2%)

NOV1 : 1  MADKPDIGEIASFNKAKLKKTEMQE~NTLLTKEAIEQEK 39 (SEQ ID NO:2)
      |||||+|||||+||||||| || ||| |||||
Sbjct: 6  MADKPDMEIASFDKAKLKKTTETQEKNTLPTKETIEQEK 45 (SEQ ID NO:34)
```

Table 3 on page 9 has been amended as follows:

Table 3.

Multiple Sequence alignment of a NOV1 polypeptide and the thymosin beta family

(Black outlined amino acids indicate potential regions of conserved sequence; grayed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs. Sequences may be referenced by the SWISSPROT or TREMBL ID.)

| | 10 | 20 | 30 | 40 | |
|----------------------------|--|--------------|----|----|----------------|
| thymosin beta family motif | | KLKKTTETQE~N | | | (SEQ ID NO:35) |
| NOV1 (2-38) | ADKPDIGEIASFNKAKLKKTEMQE~NTLLTKEAIEQEK | | | | (SEQ ID NO:2) |
| TYB0_HUMAN(1-38) | ADKPDMEIASFDKAKLKKTTETQEKNTLPTKETIEQEK | | | | (SEQ ID NO:36) |
| TYB9_BOVIN(1-40) | ADKPDLEGEINSFDKAKLKKTTETQEKNTLPTKETIEQEKQA | | | | (SEQ ID NO:37) |
| TYB9_PIG(1-40) | ADKPDMEIEKFDKSKLKKTTETQEKNTLPTKETIEQEKQA | | | | (SEQ ID NO:38) |
| TYB4_HUMAN(1-40) | SDKPDMAEIEKFDKSKLKKTTETQEKNTLPSKETIEQEKQA | | | | (SEQ ID NO:39) |
| TYB4_MOUSE(7-47) | MSDKPDMAEIEKFDKSKLKKTTETQEKNTLPSKETIEQEKQA | | | | (SEQ ID NO:40) |
| TYB4_RABIT(1-40) | ADKPDMAEIEKFDKSKLKKTTETQEKNTLPSKETIEQEKQA | | | | (SEQ ID NO:41) |
| TYB4_XENLA(1-39) | SDKPDMAEIEKFDKAKLKKTTETQEKNTLPSKETIEQEKQ~ | | | | (SEQ ID NO:42) |
| TYBY_HUMAN(1-40) | SDKPCMAEIEKFDKSKLKKTTETQEKNTLPSKETIEQEKQA | | | | (SEQ ID NO:43) |
| TYBA_ONCMY(1-40) | SDKPNLEEVASFDKAKLKKTTETQEKNTLPSKETIEQEKQA | | | | (SEQ ID NO:44) |
| TYBB_ONCMY(1-40) | SDKPDLEAEVSFDDKAKLKKTTETQEKNTLPSKETIEQEKQA | | | | (SEQ ID NO:45) |
| TYBB_LATJA(1-40) | ADKPDISEVTSFDKAKLKKTTETQEKNTLPSKETIEQEKQA | | | | (SEQ ID NO:46) |
| P97563_RAT(1-39) | MSDKPDLSEVETFDKSKLKKTTETQEKNTLPSKETIEQEK~ | | | | (SEQ ID NO:47) |
| TYBN_HUMAN(1-38) | ADKPDLEAEVDFDKSKLKKTTETQEKNTLPSKETIEQEK~ | | | | (SEQ ID NO:48) |
| O97428_DROME(95-129) | LAGIENFDKAKLKKTTETQEKNTLPSKETIEQEKQA | | | | (SEQ ID NO:49) |
| O97428_DROME(59-89) | GIATFNQNNLKKTTETQEKNTLPSKETIEQEK~ | | | | (SEQ ID NO:50) |

Table 4 on page 10 has been amended as follows:

Table 4.

PFAM alignment of a NOV1 polypeptide to the consensus sequence of the thymosin beta family

```
>PD005116 (Closest domain: TYB0_HUMAN 1-38)
Number of sequences in family: 16
Most frequent protein names: TYB4(4) TYB9(2) TYBB(2)
Commentary (automatic):
    THYMOSIN ACETYLATION T-CELL DIFFERENTIATION
    IMMUNOPOTENTIATION THYMUS BETA-4 ACTIN-BINDING PROTEIN
    BETA
    Length = 38
    Score = 145 (60.9 bits), Expect = 5e-10
    Identities = 32/38 (84%), Positives = 34/38 (89%), Gaps = 1/38 (2%)

NOV1:      2 ADKPDIGEIASFNKAKLKKTEMQE-NTLLTKEAIEQEK 38 (SEQ ID NO:2)
          |||||+|||||+||||||| || || | |||||
Sbjct:     1 ADKPDMGEIASFDKAKLKKTTETQEKNTLPKETIEQEK 38 (SEQ ID NO:51)
```

Table 6 beginning on page 13 has been amended as follows:

Table 6.

Comparison between a NOV2 polypeptide and mouse ephrin type-A receptor 8 precursor

```
>ref|NP_031965.1| Eph receptor A8  
sp|O09127|EPA8_MOUSE EPHRIN TYPE-A RECEPTOR 8 PRECURSOR (TYROSINE-PROTEIN KINASE  
RECEPTOR EEK) (EPH-AND ELK-RELATED KINASE)  
gb|AAB39218.1| (U72207) Eph-and Elk-related kinase [Mus musculus]  
Length = 1004
```

Score = 3036 bits (7128), Expect = 0.0
Identities = 945/992 (95%), Positives = 964/992 (96%), Gaps = 1/992 (0%)

```
NOV2:   1    MAPARGRLPPALWVVVTAAAAATCVSAARGEVNLLDTSTIHGDWGWLTPAHGWDSINEV   60  
      ||||| || |||||||||||| ||||| ||||||||||||||||||||||||||||  
Sbjct:  1    MAPARARLSPALWVVVTAAAAA-TCVSAGRGEVNLLDTSTIHGDWGWLTPAHGWDSINEV   59  
  
NOV2:  61    DESFQPIHTYQVCNVMSPNQNNWLRTSWVPRDGARRVYAEIKFTLRDCNSMPGVLGTCKE  120  
      ||||+||| |||||||||||| ||||+||| |||||||||||||||||||||+||| |||||  
Sbjct:  60    DESFRPIHTYQVCNVMSPNQNNWLRTNWVPRDGARRVYAEIKFTLRDCNSIPGVLGTCKE  119  
  
NOV2:  121   TFNLHYLES DRDLGASTQESQFLKIDTIAADESF TGADLGVRRLKL NTEVRSVGPLSKRG  180  
      ||||+||| |||||||||||| ||||+||| |||||||||||||||||||||+||| |||||  
Sbjct:  120   TFNLHYLES DRDLGASTQESQFLKIDTIAADESF TGADLGVRRLKL NTEVRGVGPLSKRG  179  
  
NOV2:  181   FYLAFQDIGACLA ILSRIYYKKCPAMVRNLAAFSEAVTGADSSSLVEVRGQCVRHSEER  240  
      ||||| || |||||||||||| ||||| ||||||||||||||||||||||||||||  
Sbjct:  180   FYLAFQDIGACLA ILSRIYYKKCPAMVRNLAAFSEAVTGADSSSLVEVRGQCVRHSEER  239  
  
NOV2:  241   DTPKMYCSAEGEWLVPIGKCVC SAGYEERRDACVACELGFYKSAPGDQLCARCPPHS HSA  300  
      ||||| || |||||||||||| ||||| |||||||||||| ||||+||| ||||||||||||  
Sbjct:  240   DTPKMYCSAEGEWLVPIGKCVC SAGYEERRDACA CELGFYKSAPGDQLCARCPPHS HSA  299  
  
NOV2:  301   APAAQACHCDLSYYRAALDP PPSACTRPPSAPVNLIS SVNGTSVTLEWAPPLDPGGRSDI  360  
      |||| | |||||||||||| ||||+||| |||||||||||| |||||||||||| |||||  
Sbjct:  300   TPAAQTCRCDSL YYRAALDP PPSAACTRPPSAPVNLIS SVNGTSVTLEWAPPLDPGGRSDI  359  
  
NOV2:  361   TYNVCCRRC PWALS RCEACSGSTRFVPQQTSLVQASLLVANLLAHMNY SFWIEAVNGVSD  420  
      ||||| || |||||||||||| ||||| |||||||||||| ||||| |||||||||||| |||||+|||
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```
Sbjct: 360 TYNAVCRRCPWALSHCEACSGSTRFVPQQTSLAQASLLVANLLAHMNYSFWIEAVNGVSN 419
NOV2: 421 LSPEPRRAAVVNITTNQAAPSQVVVIRQERAGQTSVSLWQEPEQPNGIILEYEIKYYEK 480
|||||
Sbjct: 420 LSPEPRSAAVVNITTNQAAPSQVVVIRQERAGQTSVSLWQEPEQPNGIILEYEIKYYEK 479
NOV2: 481 DKEMQSYSTLKAVTTRATVSGLKPGTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540
|||||
Sbjct: 480 DKEMQSYSTLKAVTTRATVSGLKPGTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 539
NOV2: 541 RTIVWICLTLITGLVLLLLLLICKKRHCYSGKAFQDSDEEKMHYQNGQAPPPVFLPLHHP 600
|||||
Sbjct: 540 RTIVWICLTLITGLVLLLLLLICKKRHCYSGKAFQDSDEEKMHYQNGQAPPPVFLPLNHP 599
NOV2: 601 PGKLPEPQFYAEPHTYEEPRAGRSFTREIEASRIHIEKIIGSGDSGEVCYGRLRVPGQR 660
|||||
Sbjct: 600 PGKFPETQFSAEPHTYEEPRAGRSFTREIEASRIHIEKIIGSGESGEVCYGRLQVPGQR 659
NOV2: 661 DVPVAIKALKAGYTERQRDFLSEASIMQGFDPHPNIRLEGVVTRGRLAMIVTEYMENG 720
|||||
Sbjct: 660 DVPVAIKALKAGYTERQRQDFLSEAAIMQGFDPHPNIRLEGVVTRGRLAMIVTEYMENG 719
NOV2: 721 LDTFLRTHDGQFTIMQLVGMLRGVAGMRYLSDLGYVHRDLAARNVLVDSNLVCKVSDFG 780
|||||
Sbjct: 720 LDAFLRTHDGQFTIVQLVGMLRGVAGMRYLSDLGYIHRDLAARNVLVDGRLVCKVSDFG 779
NOV2: 781 LSRVLEDDPDAAAYTTTGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 840
|||||
Sbjct: 780 LSRALEDDPEAAAYTTTAGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 839
NOV2: 841 NMTNRDVISSVEEGYRLPAPMGCPhALHQLMLDCWHKDRAQRPRFSQIVSVLDALIRSPE 900
|||||
Sbjct: 840 NMTNQDVISSVEEGYRLPAPMGCPRALHQLMLDCWHKDRAQRPRFAHVSVLDALVHSPE 899
NOV2: 901 SLRATATVSRCPPPAFVRSFCDLRGGSGGGGGLTVGDWLDSIRMGRYRDHFAAGGYSSLG 960
|||||
Sbjct: 900 SLRATATVSRCPPPAFARSCFCDLRAGGSGNGDLTVGDWLDSIRMGRYRDHFAAGGYSSLG 959
NOV2: 961 MVLRMNAQDVRLGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:5)
|||||
Sbjct: 960 MVLRMNAQDVRLGITLMGHQKKILGSIQTMR 991 (SEQ ID NO:52)
```

Table 6A beginning on page 14 has been amended as follows:

Table 6A.
Comparison between a NOV2 polypeptide and human ephrin receptor EphA8

```
>ref|NP_065387.1| EphA8; Ephrin receptor EphA8 (eph- and elk-related kinase); Hek3;
eph-, elk-related tyrosine kinase; ephrin receptor EphA8
emb|CAB81612.1| (AL035703) dJ61A9.1 (tyrosine kinase ) [Homo sapiens]
Length = 1005
```

Score = 2054 bits (5262), Expect = 0.0
Identities = 992/992 (100%), Positives = 992/992 (100%)

```
NOV2 : 1 MAPARGRLPPALWVVTAATAAATCVSAARGEVNLLDTSTIHGDWGWLTYPAHGWDSINEV 60
|||||
Sbjct: 1 MAPARGRLPPALWVVTAATAAATCVSAARGEVNLLDTSTIHGDWGWLTYPAHGWDSINEV 60
NOV2 : 61 DESFQPIHTYQVCNVMSPNQNNWLRTSWVPRDGARRVYAEIKFTLRDCNSMPGVLGTCKE 120
|||||
Sbjct: 61 DESFQPIHTYQVCNVMSPNQNNWLRTSWVPRDGARRVYAEIKFTLRDCNSMPGVLGTCKE 120
```

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NOV2 : 121 TFNLYYLESRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTEVRSVGPLSKRG 180
[TFNLYYLESRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTEVRSVGPLSKRG]
Sbjct: 121 TFNLYYLESRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTEVRSVGPLSKRG 180

NOV2 : 181 FYLAFQDIGACLAILSLRIYYKKCPAMVRNLAAFSEAVTGADSSSLVEVRGQCVRHSEER 240
Sbjct: 181 FYLAFQDIGACLAILSLRIYYKKCPAMVRNLAAFSEAVTGADSSSLVEVRGQCVRHSEER 240

NOV2 : 241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACVACELGFYKSAPGDQLCARCPPHSHA 300
Sbjct: 241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACVACELGFYKSAPGDQLCARCPPHSHA 300

NOV2 : 301 APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISVNGTSVTLEWAPPLDPGGRSDI 360
[APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISVNGTSVTLEWAPPLDPGGRSDI]
Sbjct: 301 APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISVNGTSVTLEWAPPLDPGGRSDI 360

NOV2 : 361 TYNAVCRRCPWALSRCACSGSTRFVPQQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420
Sbjct: 361 TYNAVCRRCPWALSRCACSGSTRFVPQQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420

NOV2 : 421 LSPEPRRAAVVNITTNQAAPSQVVVIRQERAGQTSVSLWQEPEQPNGIILEYEIKYYEK 480
Sbjct: 421 LSPEPRRAAVVNITTNQAAPSQVVVIRQERAGQTSVSLWQEPEQPNGIILEYEIKYYEK 480

NOV2 : 481 DKEMQSYSTLKAVTTTRATVSGLKPGTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540
[DKEMQSYSTLKAVTTTRATVSGLKPGTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT]
Sbjct: 481 DKEMQSYSTLKAVTTTRATVSGLKPGTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540

NOV2 : 541 RTIVWICLTLITGLVVL LLLLI CKKRHCYGS KAFQDSDEEKMHYQNGQAPPPVFLPLHHP 600
Sbjct: 541 RTIVWICLTLITGLVVL LLLLI CKKRHCYGS KAFQDSDEEKMHYQNGQAPPPVFLPLHHP 600

NOV2 : 601 PGKLPEPQFYAEPHTYEEPRAGRSFTREIEASRIHIEKIIGSGDSGEVCYGRLRVPGQR 660
Sbjct: 601 PGKLPEPQFYAEPHTYEEPRAGRSFTREIEASRIHIEKIIGSGDSGEVCYGRLRVPGQR 660

NOV2 : 661 DVPVAIKALKAGYTERQRRDFLSEASIMQFDPHPNIIIRLEGVVTRGRLAMIVTEYMENG 720
Sbjct: 661 DVPVAIKALKAGYTERQRRDFLSEASIMQFDPHPNIIIRLEGVVTRGRLAMIVTEYMENG 720

NOV2 : 721 LDTFLRTHDGQFTIMQLVGMLRGVGAGMRYLSDLGYVHRDLAARNVLVDSNLVCKVSDFG 780
Sbjct: 721 LDTFLRTHDGQFTIMQLVGMLRGVGAGMRYLSDLGYVHRDLAARNVLVDSNLVCKVSDFG 780

NOV2 : 781 LSRVLEDDPDAAAYTTTGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 840
Sbjct: 781 LSRVLEDDPDAAAYTTTGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 840

NOV2 : 841 NMTNRDVISSVEEGYRLPAPMGCPHALHQLMLDCWHKDRAQRPRFSQIVSVLDALIRSPE 900
Sbjct: 841 NMTNRDVISSVEEGYRLPAPMGCPHALHQLMLDCWHKDRAQRPRFSQIVSVLDALIRSPE 900

NOV2 : 901 SLRATATVSRCPPPAFVRSCFDLRGGSGGGGGLTVGDWLD SIRMGRYRDHFAAGGYSSLG 960
Sbjct: 901 SLRATATVSRCPPPAFVRSCFDLRGGSGGGGGLTVGDWLD SIRMGRYRDHFAAGGYSSLG 960

NOV2 : 961 MVLRMNAQDVRLGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:5)
Sbjct: 961 MVLRMNAQDVRLGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:53)

The paragraph beginning at line 4 in Table 7 on page 16 has been amended as follows:

Table 7 shows multiple sequence alignment of the NOV2 ephrin type-A receptor 8-like protein of the invention, shown as AL035703 Spliced2 , with similar proteins. The various aligned proteins are as follows: AL035703 Spliced2 (SEQ ID NO:5) with several proteins: EPA8 Mouse (SEQ ID NO:54), EPA5 Human (SEQ ID NO:55) and EPA5 Chick (SEQ ID NO:56). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

The paragraph beginning at line 5 in Table 9 on page 20 has been amended as follows:

Table 9 shows sequence alignment between a NOV3 polypeptide with several members of the human fibronectin leucine repeat transmembrane family: AAF28461.1|AF169 (SEQ ID NO:57), AAF28460.1|AF169 (SEQ ID NO:58) and AAF28459.1|AF169 (SEQ ID NO:59). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

Table 9. continued on page 21 has been amended as follows:

[TABLE 9. continued] TABLE 9A:

```
>ref|NP_037412.1| fibronectin leucine rich transmembrane protein 1
gb|AAF28459.1|AF169675_1 (AF169675) leucine-rich repeat transmembrane protein FLRT1
[Homo sapiens]
Length = 674

Score = 1365 bits (3494), Expect = 0.0
Identities = 673/674 (99%), Positives = 674/674 (99%)

NOV3: 1  MVVAHPTATATTTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRC 60
      |||
Sbjct: 1  MVVAHPTATATTTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRC 60

NOV3: 61  DNGFIYCNDRGLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDE 120
      |||
Sbjct: 61  DNGFIYCNDRGLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDE 120

NOV3: 121  FPINLPRSLRELHLQDNNVRTIARDSLARIPLLEKLHLDNDSVSTVSIEEDAFADSKQLK 180
      |||
Sbjct: 121  FPINLPRSLRELHLQDNNVRTIARDSLARIPLLEKLHLDNDSVSTVSIEEDAFADSKQLK 180

NOV3: 181  LLFLSRNHLSSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRVLVDGNLLANQRIA 240
      |||
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```
Sbjct: 181 LLFLSRNHLSSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIA 240
NOV3: 241 DDTFSRLQNLTELSLVRNSLAAPPLNLPSAHLQKLYLQDNAISHIPYNTLAKMRELERLD 300
      |||
Sbjct: 241 DDTFSRLQNLTELSLVRNSLAAPPLNLPSAHLQKLYLQDNAISHIPYNTLAKMRELERLD 300
NOV3: 301 LSNNNLTTLPRLGFDDLGNLAQLLLRNNPWFCGCNLMWLRDQVVKARAAVNVVRGLMCQGP 360
      |||
Sbjct: 301 LSNNNLTTLPRLGFDDLGNLAQLLLRNNPWFCGCNLMWLRDQVVKARAAVNVVRGLMCQGP 360
NOV3: 361 EKVRGMAIKDITSEMDECFETGPQGGVANAAAKTTASNHASATTPQGSFRTLKAKRPGLR 420
      |||
Sbjct: 361 EKVRGMAIKDITSEMDECFETGPQGGVANAAAKTTASNHASATTPQGSFRTLKAKRPGLR 420
NOV3: 421 LPDSNIDYPMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWRLRGHSPAVGSI 480
      |||
Sbjct: 421 LPDSNIDYPMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWRLRGHSPAVGSI 480
NOV3: 481 TETLVQGDKTEYLLTALEPKSTYIICMVTMETSNAAYVADETPVCAKAETADSYGPTTTLN 540
      |||
Sbjct: 481 TETLVQGDKTEYLLTALEPKSTYIICMVTMETSNAAYVADETPVCAKAETADSYGPTTTLN 540
NOV3: 541 QEONAGPMASLPLAGIIGGAVALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDY 600
      |||
Sbjct: 541 QEONAGPMASLPLAGIIGGAVALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDY 600
NOV3: 601 MESGTTKDNSILEIRGPGLOMLPINPYRAKEEYVVHTIFPSNGSSLCKATHITIGYGTTRG 660
      |||
Sbjct: 601 MESGTTKDNSILEIRGPGLOMLPINPYRAKEEYVVHTIFPSNGSSLCKATHITIGYGTTRG 660
NOV3: 661 YRDGGIPDIDYSYT 674 (SEQ ID NO:7)
      |||
Sbjct: 661 YRDGGIPDIDYSYT 674 (SEQ ID NO:60)
```

The paragraph beginning at line 6 in Table 10 on page 22 has been amended as follows:

Table 10 shows sequence alignment between a NOV3 polypeptide with various fibromodulins: ACC NO: O43408 (SEQ ID NO:61), ACC NO: AP000597 (SEQ ID NO:7), ACC NO: O43155 (SEQ ID NO:62), ACC NO: O42235 (SEQ ID NO:63) and FMOD Bovin FM (SEQ ID NO:64). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)